Announcement: The CGF's genotyping services are now available to NIH researchers and NCI grantees!

The National Cancer Institute's Core Genotyping Facility (CGF) is now open to proposals from investigators from outside of the NCI, on a limited basis. The CGF assesses human genetic variation, including Single Nucleotide Polymorphisms (SNPs) and other types of genetic variation (microsatellites, insertion/deletion mutations etc) in a large number of separate population and family studies initiated by NCI investigators. Currently the CGF is utilizing five major technology platforms to assess human genetic variation:

- TaqMan™ Fluorescent 5' Nuclease cleavage,
- Primer Extension detected by Matrix Assisted Laser Deionization/Adsorption - Time of Flight (MALDI-TOF) nucleotide extension,
- Fluorescent DNA fragment analysis and sequencing detected by automated capillary electrophoresis systems,
- MGB Eclipse™ 3' Hybridization Triggered Fluorescence,
- SNPlex™ oligonucleotide ligation assay (OLA) in combination with PCR chemistry and fluorescent DNA fragment analysis.

To enhance the reporting and storage of data, as well as all CGF processes, the CGF has implemented a Laboratory Information Management System (LIMS). The CGF also continues to provide data and support for the SNP500Cancer website (http://snp500cancer.nci.nih.gov), an internationally used and recognized resource for molecular epidemiological studies in cancer and other diseases. The CGF Bioinformatics group also has developed other high-powered analysis tools available to investigators at DCEG and worldwide. The CGF can provide investigators with sample handling, candidate gene assay development, and genotyping services on a fee-for-service basis. The CGF will not be able to entertain requests whose sole purpose is to "cost compare" for genotyping services.

Scope of applications and proposal deadlines: Excess capacity work at the CGF will be approximately 15% of the total workload and on fee-for-service basis restricted to intramural NIH investigators and extramural NCI grantees. Due to the limited capacity, priority and suitability of projects will be assessed prior to commencement of work. The quarterly application deadline will be 30 days prior to the beginning of the new fiscal quarter (deadlines = December 1, March 1, June 1 and September 1 of each calendar year). All applications must be completed and submitted via the web (click here) in order to be properly processed and reviewed; there will be no exceptions for submission. Assessment criteria include the scope of work and estimated job size.

Prioritization of proposals: All projects will receive a "yes/no" qualification, based on the minimum requirements listed below.

Submitted requests must address the following requirements:

1. All studies at the CGF are restricted to human genomic DNA from anonymized (unlinked*) subjects. There are no exceptions to this requirement.
2. A minimum of 2 ug of human genomic DNA should be available immediately. If not, clear documentation must be provided to ensure that human genomic DNA will be available by the end of the upcoming quarter to guarantee completion of work within the quarter.
3. The minimum number of samples to analyzed is 92. The CGF will not entertain requests for fewer than 92 samples.
4. The minimum number of SNPs to be analyzed must exceed 10. The CGF will not entertain requests for fewer than 10 SNPs.
5. Preference is given to requests that propose to analyze genotype assays available on the CGF validated assay list (see http://snp500cancer.nci.nih.gov/assay_list.cfm). If the assays are not available, then the proposed development of assays must be targeted to the platforms at the CGF, TaqMan, MGB Eclipse, Sequenom, SNPLEX, Sequencing, or Fragment Analysis.

In addition, all "minimally qualified" projects will receive a priority score on a 1-5 scale (5 being highest). Projects with the highest priority score will be completed first; those with lower scores will be moved down in the queue for the current quarter based on the CGF workload and availability of excess capacity (not to exceed 15% overall production level). The priority score will be based on the following four criteria: scientific rationale, scientific content, study design (including sample-related issues), and feasibility. When an application is accepted, the applicant will be notified by email before the upcoming new quarter, and must: 1) Complete the Materials Transfer Agreement - to be signed and returned, 2) Agree to the Terms of Service by email acknowledgement for NIH investigators or by signing and returning the Terms of Service Agreement for NCI-grantees not at the NIH. All investigators must provide billing contacts and center or purchase order numbers for billing purposes. In the event that an application does not receive a high enough priority score, the applicant will be notified in writing within 90 days of submission of the proposal. Applications that receive a low priority score may be resubmitted for consideration in a subsequent quarter. Requests will not roll over from quarter to quarter.

*__Unlinked:__ *human data or samples that were initially collected with identifiers but, prior to research use, have been irreversibly stripped of all identifiers by use of an arbitrary or random alphanumeric code and the key to the code is destroyed, thus making it impossible for anyone to link the samples to the sources. This process does not preclude linkage with existing clinical, pathological, and demographic information before subject identifiers are removed.*

Services offered: The CGF offers the following services to qualified applicants

- Sample handling of purified human genomic DNA or whole genome amplified human genomic DNA. This includes quantification of each sample via Pico Green®, real time TaqMan®, Amelogenin sex and 15 forensic STR marker typing, which are included in the Applied Biosystems Identifiler® panel for sample identification. This is required of all samples and is not negotiable.

- Upon completion of sample handling portion of a project, the a sample handling reports will be delivered to investigators in Microsoft Excel workbooks, with a initial worksheet summary data as to the methods used to produce the report and individual worksheets for the quantification and total amount of sample provided to the CGF, and the Identifiler data (genotypes for the 15 STRs and Amelogenin sexing).

- Single Nucleotide Polymorphism (SNP) genotype analysis of human genomic DNA or whole genome amplified human genomic DNA with the selected assays are displayed on the SNP500Cancer website (http://snp500cancer.nci.nih.gov/assay_list.cfm).

- Upon completion of genotyping portion of a project, the data will be delivered to investigators in Microsoft Excel workbooks, with a initial worksheet providing link to the SNP500 cancer website to describe the SNPs genotyped and their corresponding assays conditions, and separate worksheets for each SNP providing the assay id and allele information, basic statistics of the entire DNA dataset (completion, allele frequency, genotype frequency) and for each sample the Plate ID, Well ID, CGF Sample ID, Provider Vial ID, and genotype call.

- SNP validation by resequence analysis and high-throughput genotype assay development for SNPs that have not yet been analyzed at the CGF and therefore do not appear on the SNP500Cancer website.

Pricing: The pricing structure for these services is described below:

- Every new sample (not already handled and at the CGF) is subject to a sample handling charge of 10.00 USD per sample handling charge, which includes the aliquoting of the sample, evaluation of the sample's concentration and total amount of DNA based on Pico-Green® and real-time TaqMan®, and generation of a genetic profile fingerprint (15 STR markers plus Amelogenin "Sex" determination). This is required for all samples, with no exceptions.
- All of the genotyping costs are based on using CGF "validated" assays (SNPs that have been sequenced in the SNP500Cancer N=102 population, and having assays demonstrating a greater than 95% completion rate and 100% genotype concordance between the assay-determined genotypes and the sequencing-determined genotypes for the SNP500Cancer population); a list of these is available on the SNP500Cancer website at http://snp500cancer.nci.nih.gov/assay_list.cfm.

	Number Of Samples...			
Number of SNPs	**92-500***	**501-1200**	**1201-3000**	**3000**
10-50	$1.75	$1.25	$1.00	$0.85
51-100	$1.50	$1.00	$0.85	$0.65
>100	$1.25	$0.85	$0.65	$0.50

* The CGF will not entertain requests for genotyping fewer than 92 samples

SNP assays that are not validated can be requested, but are subject to a 400.00 USD assay development charge if the SNP has been sequenced in the SNP500Cancer population, or a 1,000.00 USD sequencing and assay development charge if the SNP has not been sequenced in the SNP500Cancer population.

NOTE: All requests submitted through this mechanism will be subject to a fee of 27.82% to reimburse NCI management and support costs.

Required documents: Successful applicants will be required to complete the following documents:

- Material Transfer Agreement (MTA)
- Terms of Service (TOS)